

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 25.6395 Seconds
(without alignments)
843.812 Million cell updates/sec

Title: us-09-622-613b-8

Perfect score: 582

Sequence: 1 MDWLTFQKKHLTNTROVDC.....TFCVTCENQAPVHVGVC 105

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	96.2	127	13	Q918V8 rana pipien
2	538	92.4	127	13	Q8U0V5 rana pipien
3	386.5	66.4	129	13	Q9DFY6 rana catesb
4	371	63.7	128	13	Q9DFY8 rana catesb
5	296	50.5	128	13	Q9DFY7 rana catesb
6	294	50.5	128	13	Q9DFY5 rana catesb
7	283	48.6	133	13	Q98SM0 rana catesb
8	277	47.6	133	13	Q9PMK7 rana catesb
9	271	46.6	133	13	Q9SLI9 rana catesb
10	270	46.4	132	13	Q98SM2 rana catesb
11	267	45.9	133	13	Q98SM8 rana catesb
12	265	45.5	132	13	Q98SM1 rana catesb
13	260.5	44.8	132	13	Q9DFY8 rana catesb
14	149.5	25.7	169	13	Q9W738 xenopus lae
15	119	20.4	157	11	Q9JKJ3 meriones un
16	119	20.4	157	11	Q9JKI9 meriones un

17	117	20.1	152	11	Q9JKI5 mus saxicol
18	117	20.1	157	11	Q9JKI4 meriones un
19	114.5	19.7	153	11	Q9JKI7 mus saxicol
20	114	19.6	157	11	Q9JKI2 meriones un
21	114	19.6	157	11	Q9JKI1 meriones un
22	112.5	19.3	132	6	Q9TV24 galago moho
23	111	19.1	154	11	Q9JKI8 mus saxicol
24	108.5	18.6	155	11	Q9JKI9 mus pahari
25	107.5	18.5	119	6	Q9TV32 gorilla gor
26	107.5	18.5	132	6	Q9TV25 indurur ful
27	107.5	18.5	155	11	Q9JKI3 mus saxicol
28	106.5	18.3	119	6	Q9TS06 cercoptithec
29	106.5	18.3	119	6	Q9TV30 saguinus oe
30	105.5	18.1	155	11	Q9JKI8 mus pahari
31	105	18.0	124	6	Q9TSF2 bos taurus
32	105	18.0	136	11	Q923I6 mus musculu
33	104.5	18.0	155	11	Q9JKI6 mus saxicol
34	104	17.9	124	6	Q95NE6 bubalus bub
35	103.5	17.8	155	11	Q9R134 ratus norv
36	103.5	17.8	155	11	Q9JKI4 mus saxicol
37	103.5	17.8	155	11	Q9JKI2 mus saxicol
38	102.5	17.6	170	6	Q9BEC1 treagus ja
39	102	17.5	144	6	Q9BH14 antilocapra
40	102	17.5	156	11	Q9JKI7 mus caroli
41	102	17.5	156	11	Q9JKI6 mus caroli
42	101.5	17.4	155	11	Q9R125 mus musculu
43	101	17.4	156	11	Q9JKI7 mus caroli
44	101	17.4	156	11	Q9VHS0 mus musculu
45	100.5	17.3	119	6	Q9TV31 salmifl sci

ALIGNMENTS

RESULT 1

ID	Q918V8	PRELIMINARY:	PRT:	127 AA.
AC	Q918V8:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Onconase variant repURL precursor.			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.			
OX	NCBI_Taxid=8404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=20330357; PubMed=10871370;			
RA	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;			
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a			
RT	3' UTR of unusual length and structure."			
RL	Nucleic Acids Res. 28:2375-2382(2000).			
DR	EMBL; AF165133; AAF76935.1;			
DR	HSSP; P22069; IONC.			
DR	InterPro; IPR001427; RNaseA.			
DR	PIfam; PF00074; rnasea; 1.			
DR	ProDom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL 1 23			POTENTIAL.
SQ	SEQUENCE 127 AA: 14491 MW: 8511DC5407AB69B CRC64;			
QY	Query Match	96.2%;	Score 560;	DB 13; Length 127;
DB	Best Local Similarity	97.1%;	Pred. No. 8.9e-57;	
	Matches 101;	Conservative 1;	Mismatches 2;	Indels 0; Gaps 0;
	2	ODWLTFQKKHLTNTROVDCNNILSTNLFHCKDKNTFTTSRPPVAKICKGIASNVLT 61		
	24	ODWLTFQKKHLTNTROVDCNNILSTNLFHCKDKNTFTTSRPPVAKICKGIASNVLT 83		

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OY 62 FEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 105
DB 84 SEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 127

RESULT 2
O8UVX5 ID O8UVX5 PRELIMINARY: PRT: 127 AA.
AC O8UVX5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Oncocase precursor.
GN RPR.
OC Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF32139; AAL54383.1;
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA: 14469 MW: 953F90D351CFEEF3 CRC64;

Query Match
Best Local Similarity 92.4%; Score 538; DB 13; Length 127;
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 QDMLEFQKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPKAICKGIISKVLT 61
DB 24 QDMLEFQKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPKAICKGIISKVLT 83
OY 62 FEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 105
DB 84 SEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 127

RESULT 3
Q9DFY6 ID Q9DFY6 PRELIMINARY: PRT: 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC MEDLINE=20512555; PubMed=11058105;
RX Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242555; AAC31441.2;
DR HSP: P22069; IONC.

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DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA: 14724 MW: 826A62882B10ABDA CRC64;

Query Match
Best Local Similarity 66.4%; Score 386.5; DB 13; Length 129;
Matches 68; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

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OY 2 QDMLEFQKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPKAICKGIISKVLT 61
DB 24 QDMLEFQKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPKAICKGIISKVLT 83
OY 62 FEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 105
DB 84 SEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 127

RESULT 4
Q9DFY8 ID Q9DFY8 PRELIMINARY: PRT: 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC MEDLINE=20512555; PubMed=11058105;
RX Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242553; AAC31439.1;
DR HSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA: 14839 MW: 989719CF52053ECC CRC64;

Query Match
Best Local Similarity 63.7%; Score 371; DB 13; Length 128;
Matches 68; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

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OY 2 QDMLEFQKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPKAICKGIISKVLT 61
DB 24 QDMLEFQKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPKAICKGIISKVLT 83
OY 62 FEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 105
DB 84 DEFLSDCNVTSRPPCKYKLLKSTTFCVTCENQAPVHFVGHC 127

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DR	Pfam: PF00074; rnaaseA; 1.
DR	ProDom: PD000535; rnaaseA; 1.
DR	SMART: SM00092; RNase_Pc; 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
FT	SIGNAL
SO	SEQUENCE 128 AA: 14804 MW: AEBBPD67D266C7C2 CRC64;
	POTENTIAL.
	RC-RNASE6_RIBONUCLEASE.
	AEBBPD67D266C7C2 CRC64;
Query Match	50.5%; Score 294; DB 13; Length 128;
Best Local Similarity	51.9%; Pred. No. 3; Gaps 0;
Matches 54; Conservative 14; Mismatches 36; Indels 0; Caps 0:	
OY	2 QDWLTFOKKHLINTRDVDCNNILSTNLNFHCKDKNTFIYSRPPVKAICGIIASKNVLTT 61 : : : :
DB	24 QDWTFQKHKHTLDFRKVKCDVMKKALFDCKRTFTIFARPPVQAQLCKNIKIDMTNVLSR 83 : : : :
OY	62 FEETISDCNVTNRPCPKYLKKSTTFCVTCENQAPVHFVGSHC 105 : : : :
DB	84 DVFLTPCCNKRRKLPCRHRDSDTNITCLTKMKELPHFAGVGKC 127 : : : :
RESULT 7	
ID	098SMO PRELIMINARY; PRT; 133 AA.
AC	098SMO:
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Rnase A-type ribonuclease rc208 precursor.
OC	Rana catesbeiana (bull frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranae.
RN	NCB1_TaxID=8400;
RE	SEQUENCE FROM N.A.
RX	MEDLINE=21539506; PubMed=11683320;
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT	"Rapid diversification of RNase A superfamily ribonuclease from the
RL	bullfrog, Rana catesbeiana.";
J	J. Mol. Evol. 53:31-38(2001);
DR	EMBL: AF351209; AAA30255.1;-
DR	HSSP; P11916; IBC4.
DR	InterPro: IPRO01427; RNaseA.
DR	Pfam: PF00074; rnaaseA; 1.
DR	ProDom: PD000535; RNaseA; 1.
DR	SMART: SM00092; RNase_Pc; 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
FT	SIGNAL
SO	SEQUENCE 133 AA: 14628 MW: 87FCEFL22C3499E02 CRC64;
	POTENTIAL.
	RC-RNASE6_RIBONUCLEASE.
	87FCEFL22C3499E02 CRC64;
Query Match	48.6%; Score 283; DB 13; Length 133;
Best Local Similarity	47.7%; Pred. No. 6; Gaps 3;
Matches 53; Conservative 16; Mismatches 34; Indels 8; Caps 3:	
OY	2 QDWLTFOKKHLINTRDVDCNNILSTNLNFHCKDKNTFIYSRPPVKAICGIIASKNVL 57 : : : :
DB	23 QNWAFQCKHITNTSIINCNTIMDNIIIVGGCGGVNTFFIISATYKAICTGYI-NMN 81 : : : :
OY	58 VLTTFEFLSDC--NVTSRPCPKYLKKSTTFCVTCENQAPVHFVGSHC 105 : : : :
DB	82 VLSTTRFOLNCTRTSIPRCPYPSSPTENNVIYCVKCNQYVPHFAGIGKC 132 : : : :
RESULT 8	
ID	09PWRT PRELIMINARY; PRT; 133 AA.
AC	09PWRT:
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Ribonuclease precursor.

GN RCR.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=98165825; PubMed=9497370;
 RA Huang H.C., Wang S.C., Liao Y.J., Lu S.C., Liao Y.D.;
 RT "The Rana catesbeiana rcr gene encoding a cytototoxic ribonuclease.
 RT Tissue distribution, cloning, purification, cytotoxicity, and active
 RT residues for RNase activity.";
 RL J. Biol. Chem. 273:6395-6401(1998).
 DR EMBL: AF039104; AAD10702.1; -
 DR HSSP: P11916; 1BC4
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT CHAIN 1 22 POTENTIAL.
 FT SIGNAL 23 133 RIBONUCLEASE.
 SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 47.6%; Score 277; DB 13; Length 133;
 Best Local Similarity 47.7%; Pred. No. 3,4e-24;
 Matches 53; Conservative 16; Mismatches 34; Indels 8; Gaps 3;

OY 2 QDWLTFQKHLLNTRDVCNNILSTNLF---HCKDKNTFYSRPEPVKAICKGIASKN 57
 DB 23 QWMAFFQCKHINTPTINCNTIMDNNTIYVGQCKRVNFTIISATYKALCTGVI-MKN 81
 OY 58 VLTTFEFLSDC---NWTSPCKYKLLKSTTFECVTCENQAPVHFGVGHG 105
 DB 82 VLSSTKFDLCTRTSITPCCPYSSKRTETNYICVKCENQPVHFGAGIGRC 132

RESULT 9

O98SL9 PRELIMINARY; PRT; 133 AA.

AC O98SL9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc212 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351210; AAK30256.1; -
 DR HSSP: P11916; 1BC4
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 46.6%; Score 271; DB 13; Length 133;
 Best Local Similarity 45.9%; Pred. No. 1.6e-23;
 Matches 51; Conservative 17; Mismatches 35; Indels 8; Gaps 3;

OY 2 QDWLTFQKHLLNTRDVCNNILSTNLF---HCKDKNTFYSRPEPVKAICKGIASKN 57
 DB 23 QWMAFFQCKHINTPTINCNTIMDNNTIYVGQCKRVNFTIISATYKALCTGVI-MKN 81
 OY 58 VLTTFEFLSDC---NWTSPCKYKLLKSTTFECVTCENQAPVHFGVGHG 105
 DB 82 VLSSTKFDLCTRTSITPCCPYSSKRTETNYICVKCENQPVHFGAGIGRC 132

RESULT 10

O98SM2 PRELIMINARY; PRT; 132 AA.

AC O98SM2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351207; AAK30253.1; -
 DR HSSP: P11916; 1BC4
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT CHAIN 23 132 RC-RNASE7.
 FT SIGNAL 1 22 POTENTIAL.
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 46.4%; Score 270; DB 13; Length 132;
 Best Local Similarity 45.9%; Pred. No. 2.1e-23;
 Matches 51; Conservative 14; Mismatches 38; Indels 8; Gaps 3;

OY 2 QDWLTFQKHLLNTRDVCNNILSTNLF---HCKDKNTFYSRPEPVKAICKGIASKN 57
 DB 23 QWMAFFQCKHINTPTINCNTIMDNNTIYVGQCKRVNFTIISATYKALCTGVI-MKN 81
 OY 58 VLTTFEFLSDC---NWTSPCKYKLLKSTTFECVTCENQAPVHFGVGHG 105
 DB 82 VLSSTKFDLCTRTSITPCCPYSSKRTETNYICVKCENQPVHFGAGIGRC 132

RESULT 11

O98SL8 PRELIMINARY; PRT; 133 AA.

AC O98SL8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc218 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.

RESULT 13

RESULT 14

RN	[2]
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SEQUENCE FROM N. A.
Kirschner M W
Kioshita N
BA

